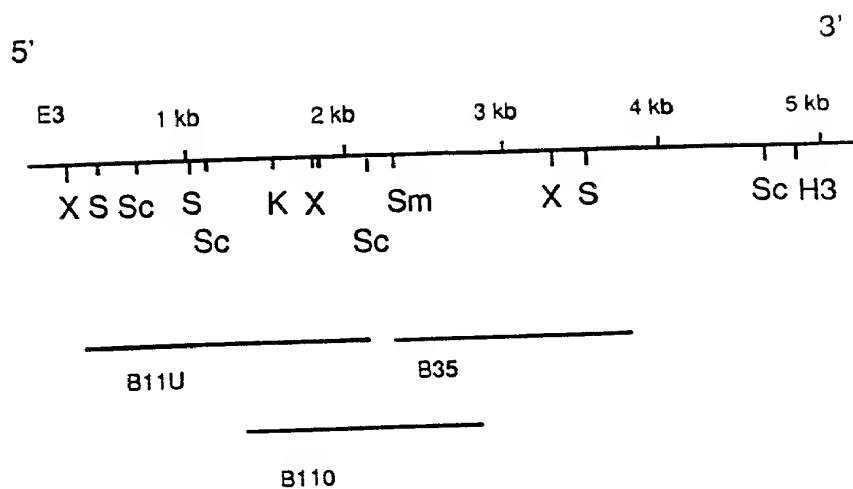


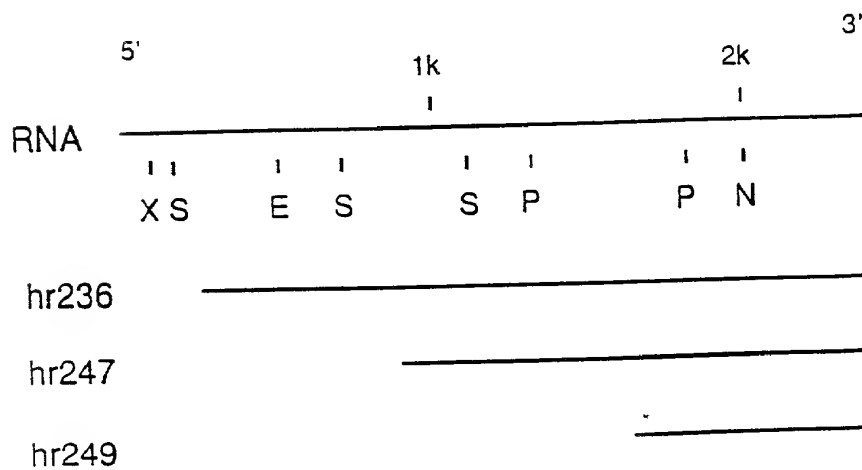
Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

FIG. 1a

Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1, X=Xho1

FIG. 1b

10 30 50
 GTTCTGCCCTCCCGACGGTAATAATAGGGGAACAATGTACGCCGAAAGCGACAGACGTG
 -----+-----+-----+-----+-----+-----+-----+
 M Y A K A T D V
 replicase start
 70 90 110
 GCGGTGTCTACGCCGGCAGATGTGCCCTACGCCAACGTACTGCAGCAGAGAGCAGTC
 -----+-----+-----+-----+-----+-----+-----+
 A R V Y A A A D V A Y A N V L Q Q R A V
 130 150 170
 AAGTTGGACTTCGCCCGCCCACTGAAGGCACCTAGAAACCCCTCCACAGACTGTACTATCCG
 -----+-----+-----+-----+-----+-----+-----+
 K L D F A P P L K A L E T L H R L Y Y P
 190 210 230
 CTGCGCTTCAAAGGGGCACTTTACCCCGACACACAACCCGATCCTGGCCGGCACCAA
 -----+-----+-----+-----+-----+-----+-----+
 L R F K G G T L P P T Q H P I L A G H Q
 250 270 290
 CGTGTGCAGAGAGGTTCTGCACAAATTTCGCCAGGGGACGTAGCACAGTCTCGAGATA
 -----+-----+-----+-----+-----+-----+-----+
 R V A E E V L H N F A R G R S T V L E I

310	330	350
GGGCCGTCTG	CACAGCGCACTTAAGCTACATGGGGCACCGAACGCCCCCGTCGCAGAC	
-----+	-----+	-----+
G P S L H S A L K L H G A P N A P V A D		
370	390	410
TATCACGGGTGCACCAAGTACGGCACCCGCGACGGCTCGCGACACATTACGGCCTTAGAG		
-----+	-----+	-----+
Y H G C T K Y G T R D G S R H I T A L E		
430	450	470
TCTAGATCCGTGCGCACAGGCCGGCCCGAGTTCAAGGCCGACCGCCTCACTGCTCGCCAAC		
-----+	-----+	-----+
S R S V A T G R P E F K A D A S L L A N		
490	510	530
GGCATTGCCCTCCCGCACCTTCTGCGTCGACGGAGTCGGCTCTTGCGCGTTCAAAATCGCGC		
-----+	-----+	-----+
G I A S R T F C V D G V G S C A F K S R		
550	570	590
GTTGGAATGCCAATCACTCCCTCTATGACGTGACCCCTAGAGGAGCTGGCCAATGCGTTT		
-----+	-----+	-----+
V G I A N H S L Y D V T L E E L A N A F		

FIG. 2 Cont'd

2410 2430 2450
CAGGAGGAAAGTCGCGCCACGGGGCTGAGGGCGGATGACTGTGCACGAAGCGCAGGGA
-----+-----+-----+-----+-----+-----+-----+
Q E E K S R H G A E G A M T V H E A Q G
2470 2490 2510
CGCACTTTTGGCTGTCTGCTATTCTGCAATACACGGCTCCACAGCAGCAGAAGCTCCTC
-----+-----+-----+-----+-----+-----+-----+
R T F A S V I L H Y N G S T A E Q K L L
2530 2550 2570
GCTGAGAAAGTCGCACCTTCTAGTCGGCATCACGCGCCACACCAACCCTGTACATCCGC
-----+-----+-----+-----+-----+-----+-----+
A E K S H L L V G I T R H T N H L Y I R
2590 2610 2630
GACCCGACAGGTGACATTGAGAGACAATCAACCATAGCGCGAAAGCCGAGGTGTTACA
-----+-----+-----+-----+-----+-----+-----+
D P T G D I E R Q L N H S A K A E V F T
2650 2670 2690
GACATCCCTGCACCCCTGGAGATCACGACTGTCAAACCGAGTGAAGAGTGCAGCGCAAC
-----+-----+-----+-----+-----+-----+-----+
D I P A P L E I T T V K P S E E V Q R N

4210 4230 4250
GCAGGTTTCGTTCGACATGTGGAAGCCGGAACGCCCTTCTCACTTACCGCGAAAGCT
-----+-----+-----+-----+-----+-----+-----+
A G F V A T C A K P E T P S S L T A K A
M C E A G N A F F T Y R E S W
P11a start
4270 4290 4310
GGTGTTCGCGACTACAAGCCACGTTGCGACTGGGACTGCGCCCCCGGAGTCTCCATGG
-----+-----+-----+-----+-----+-----+-----+
G V S A T T S H V A T G T A P P E S P W
C F C D Y K P R C D W D C A P G V S M G
4330 4350 4370
GATGCACCTGCAGCCAACAGCTTTTCGGAGTTATTGACACCGGAGACCCCGTCCACATCA
-----+-----+-----+-----+-----+-----+-----+
D A P A A N S F S E L L T P E T P S T S
C T C S Q Q L F G V I D T G D P V H I I
4390 4410 4430
TCCTCGCCGTCATCGTCTTCATCGGACTCCCTCTACATCGTGTGAAGTCCGCTCAGTGGT
-----+-----+-----+-----+-----+-----+-----+
S S P S S S S D S S T S C G R S L S G
L A V I V F I G L L Y I V W K V A Q W W

FIG. 2 Cont'd

4450 4470 4490
GGAGACACCGCAAGGACCACAGAGACTTGAAACAGCAGAAAGCCGCTTCGCAAGACAGG
-----+-----+-----+-----+-----+-----+-----+-----+
G D T A R T T E D L N S R K P P S Q D R
R H R K D H R R L E Q Q K A A F A R Q A

4510 4530 4550
CAATCACGCTCGTCTGAATGTCTGGACAGAGCGGAGAAAGGACAGGCAGTTCGTTAACT
-----+-----+-----+-----+-----+-----+-----+
Q S R S S E C L D R S G E R T G S S L T
I T L V * M S G Q K R R K D R Q F V N C
P11b start

4570 4590 4610
GCCCCACTGCTCCGAGCCCTCATTCATTTTCGGAAGAGCTCGACTGCCGCCGGG
-----+-----+-----+-----+-----+-----+-----+
A P T A P S P S F S F S E R A R L A T G
P H C S E P L I L I F G K S S T G D R A

4630 4650 4670
CCGACTGTGCGCGTGGACATCACCTTCGGCAACCCATCTGCGCCACGACCAAGTT
-----+-----+-----+-----+-----+-----+-----+
P T V A A A T S P S A T P S C A T D Q V
D C R R C D I T F G N P I L R H G P G C

	4690		4710		4730
GCCGCGAGGACCA	GCGCGACTT	TGCGCCTT	CCTGGTT	CCCAGTCT	GCCCCGTGCTGTC
A A R T T P D F A P F L G S Q S A R A V	R E D H A G L C A F P G F P V C P C C L				
TCGAAGCCGTAC	CGGCCCCACG	ACTGCCCGT	TGGAAGA	AGTCA	CCCCGCTCCACGC
S K P Y R P P T T A R W K E V T P L H A	E A V P A P H D C P L E R S H P A P R V				
TGGAAGGCGTG	ACCGGAGACC	GACCGAAGT	CAGGAGG	ACCCGGAG	ACAGCGCGGTC
W K G V T G D R P E V R E D P E T A A V	E G R D R R P T G S Q G P G D S G G R				
GTCCAGGCTCT	GATCAGCGG	CGTTATCCT	CAGAAG	ACGAGCTT	CCTCCGACGATCC
V Q A L I S G R Y P Q K T K L S S D A S	P G S D Q R P L S S E D E A F L R R I Q				


```

370                               390                               410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAAACCGTCGCGGAACCCGTA
-----+-----+-----+-----+-----+-----+-----+
A G W E M L E W R H S D L T T V A E P V
      M G D A G V A S Q R P H N R R G T R N
      P71 start

430                               450                               470
ACGTTGCGGTGAGCGCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGCGTCGGA
-----+-----+-----+-----+-----+-----+-----+
T F G S A P T P S P S M V E E T N G V G
      V R V S A N T V T V N G R R N Q R R R T

490                               510                               530
CCGGAAGGCAAGTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAA
-----+-----+-----+-----+-----+-----+-----+
P E G K F L P L T I S P L L H K T S R K
      G R Q V S P P D N F T A A A Q D L A Q S

550                               570                               590
GCCTTGACGCCAACACCGTCACTTCCCCCGCTAACATCTCTAGCATGCCCGAATTCGGA
-----+-----+-----+-----+-----+-----+-----+
A L T P T P S L S P L T S L A C P N S G
      L D A N T V T F P A N I S S M P E F R N

```

FIG. 3a Cont'd

850	870	890
CCTTTCGGATGTT	CAGAACCGCCT	ACGTCGCCGT
AGCGGCTAGCG	AACGTCGAG	AACAAGGAGATGT
-----+	-----+	-----+
F	P	M
F	R	T
A	Y	V
A	V	A
N	V	E
N	K	E
M	S	
910	930	950
CGCTCGACGTTGT	CAACGACCTCAT	CGAGTGGCTCA
CAACGACCTCAT	CGAGTGGCTCA	CAATCTGCCGACT
GGCGTTATG	-----+	-----+
L	D	V
V	N	D
L	I	E
W	L	N
N	L	A
D	W	R
Y	V	
970	990	1010
TCGTTGACTCTGA	CAGTGGATTAACT	TCACTTCA
CACTTCACTTCA	CAATGACAC	CACTACTACGTC
CGCATCC	-----+	-----+
V	D	S
E	Q	W
I	N	F
T	N	D
T	Y	Y
V	R	I
R		
1030	1050	1070
GCGTTCTACGTCC	AACCTACGACGTT	CCAGACCCAC
AGAGGCCCTTGT	TCGCACAGTCT	-----+
V	L	R
P	T	Y
D	V	P
D	P	T
E	G	L
V	R	T
V	S	
1090	1110	1130
CAGACTACCGCCT	CACCTTATAAGGCG	ATAACATGTGA
AGCCAACATG	CCAACTCGTCG	-----+
D	Y	R
L	T	Y
K	A	I
T	C	E
A	N	M
P	T	L
V	D	

1150 1170 1190
ACCAAGGCTTTGGATCGGGCCAGTACGCTCTCACCCTAGCTACCGCAGTACG
-----+-----+-----+-----+-----+-----+-----+
Q G F W I G G Q Y A L T P T S L P Q Y D
1210 1230 1250
ACGTCAGCGAGGCCCTACGCTCTGCACACTTTGACCTTGCCAGACCATCCAGCGCCGCTG
-----+-----+-----+-----+-----+-----+-----+
V S E A Y A L H T L T F A R P S S A A A
1270 1290 1310
CACTCGCGTTTGTGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCAG
-----+-----+-----+-----+-----+-----+-----+
L A F V W A G L P Q G G T A P A G T P A
1330 1350 1370
CCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCCTGGGCCACAACGGTACTATTCC
-----+-----+-----+-----+-----+-----+-----+
W E Q A S S G G Y L T W R H N G T T F P
1390 1410 1430
CAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCGA
-----+-----+-----+-----+-----+-----+-----+
A G S V S Y V L P E G F A L E R Y D P N

2050 2070 2090
CCGACGACCTGGCCACCCGCTCACAGGTGTCTACCCGCCACTGACAACTTCGCGGCCG
-----+-----+-----+-----+-----+-----+-----+
D D L A T R L T G V Y P A T D N F A A A
2110 2130 2150
CCGTTTCTGCCTTCGCCGCGAACAATGCTGTCTCCTCCGTGCTGAAGTCGGAGGCAACGTCCT
-----+-----+-----+-----+-----+-----+-----+
V S A F A A N M L S S V L K S E A T S S
2170 2190 2210
CCATCATCAAGTCCGTTGGCGAGACTGCCGTGGCGGCGCTCAGTCGGCCTCGCGAAGC
-----+-----+-----+-----+-----+-----+-----+
I I K S V G E T A V G A A Q S G L A K L
2230 2250 2270
TACCCGACTGCTAATGAGTGACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCCGAG
-----+-----+-----+-----+-----+-----+-----+
P G L L M S V P G K I A A R V R A R R A
2290 2310 2330
CGCGCCGCGCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTCGCCGTTTCGTAA
-----+-----+-----+-----+-----+-----+-----+
R R R A A R A N *

FIG. 3 a Cont'd

2350 2370 2390
ACGGCGTGGTCCCGCACATTAACGCTACCCCTAAAGACTCTGGTGAGTCCCCCGTCGTTACA
-----+-----+-----+-----+-----+-----+-----+
2410 2430 2450
CGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAAGACGTAGTTAGCTCT
-----+-----+-----+-----+-----+-----+-----+
2470
GCGTCCCTCGGGATACCA
-----+-----+-----+-----+-----+-----+-----+

FIG. 3a Cont'd

```

10          30          50
GTTTTCCTTACCAAGTGTGGTAAATTTAAACAAGAAAGAACGACCGTAA
-----+-----+-----+-----+-----+-----+
70          90          110
CCCGGCCCTTACACCTCGAGTCCGTGACCACCGGATTATACGTCGCCACACACGGC
-----+-----+-----+-----+-----+-----+
130         150         170
GCCTTTCCGACCACTCTCGAGAGTCGTTGGAGTTTCGTCCTGACCAACCGGTGGCA
-----+-----+-----+-----+-----+-----+
190         210         230
GTCGACAGACGCTTCCGGACCACTAGAACCCTCTCGAGCGACACACACACACA
-----+-----+-----+-----+-----+-----+
250         270         290
CCGCCCTAGCTGCACCTACGGCAGCGTTGATAGCGCGGATTATAGCGGACACCATC
-----+-----+-----+-----+-----+-----+
310         330         350
GCCCACTCCATCACAATTACCAACCCGGTTACACCCCTTGCCCTAATACCCCTGAACCTGAA
-----+-----+-----+-----+-----+-----+
A H S I T L P P G Y T L A L I P P E P E

```

M S E H T I
"P70" fusion protein start

Fig. 3b

970	990	1010
GTCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACTAGTACTACGTCGCCATC		
-----+	-----+	-----+
V V D S E Q W I N F T N D T T Y Y V R I		
1030	1050	1070
CGCGTTCTACGTCCAACCTACGACGTTCCAGACCCACAGAGGGCCTTGTTGCGACAGTC		
-----+	-----+	-----+
R V L R P T Y D V P D P T E G L V R T V		
1090	1110	1130
TCAGACTACCGCCTCACTTATAAGGCGGATAACATGTGAAGCCAACATGCCAACACTCGTC		
-----+	-----+	-----+
S D Y R L T Y K A I T C E A N M P T L V		
1150	1170	1190
GACCAAGGCTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTAC		
-----+	-----+	-----+
D Q G F W I G G Q Y A L T P T S L P Q Y		
1210	1230	1250
GACGTCAGCGAGGCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCGCT		
-----+	-----+	-----+
D V S E A Y A L H T L T F A R P S S A A		

Fig. 3b (cont'd)

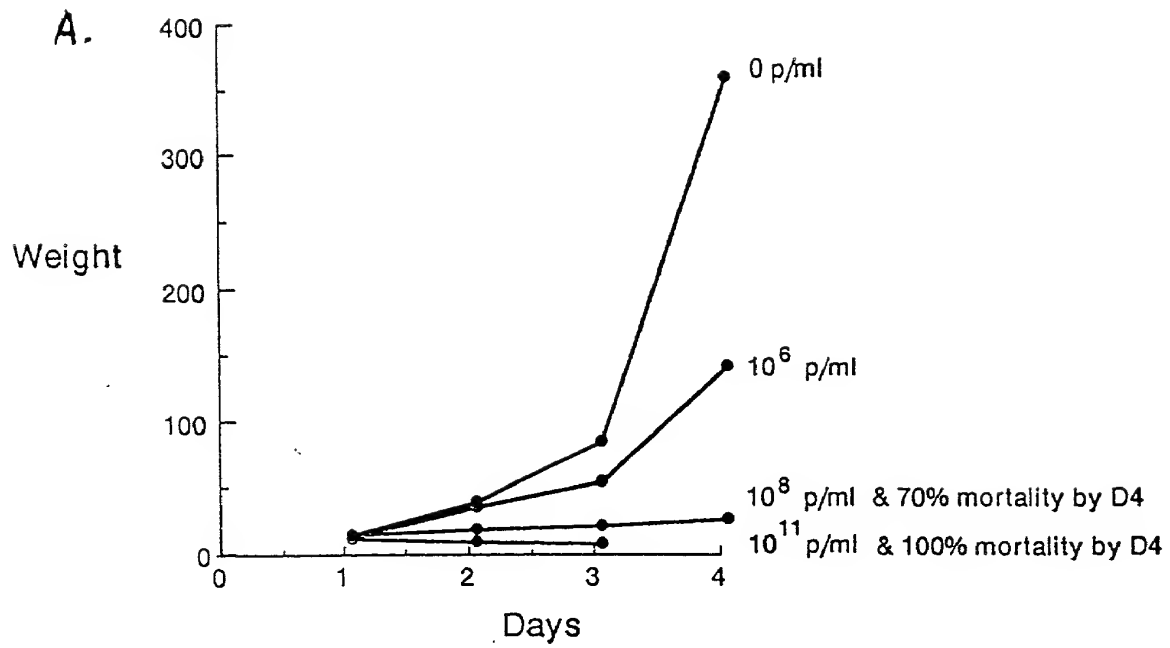
1270 1290 1310
GCACTCGCGTTTGTGTGGCAGGTTTGCCACACAGGTGGCAGTGCCTGCAGGCACTCCA
-----+-----+-----+-----+-----+-----+-----+
A L A F V W A G L P Q G G T A P A G T P
1330 1350 1370
GCCTGGGAGCAGGCACTCTGGGTGGTACCTCACCTGGCGCCACAACGGTACTATTTC
-----+-----+-----+-----+-----+-----+-----+
A W E Q A S S G G Y L T W R H N G T T F
1390 1410 1430
CCAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCG
-----+-----+-----+-----+-----+-----+-----+
P A G S V S Y V L P E G F A L E R Y D P
1450 1470 1490
AACGACGGCTCTTGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTCCGGCAGGTC
-----+-----+-----+-----+-----+-----+-----+
N D G S W T D F A S A G D T V T F R Q V
1510 1530 1550
GCCGTCGACGAGTCTGTGTGACCAACAACCCCGCGCGGCGGAGCGCCCCACCTTC
-----+-----+-----+-----+-----+-----+-----+
A V D E V V V T N N P A G G S A P T F

Fig. 3b (cont'd)

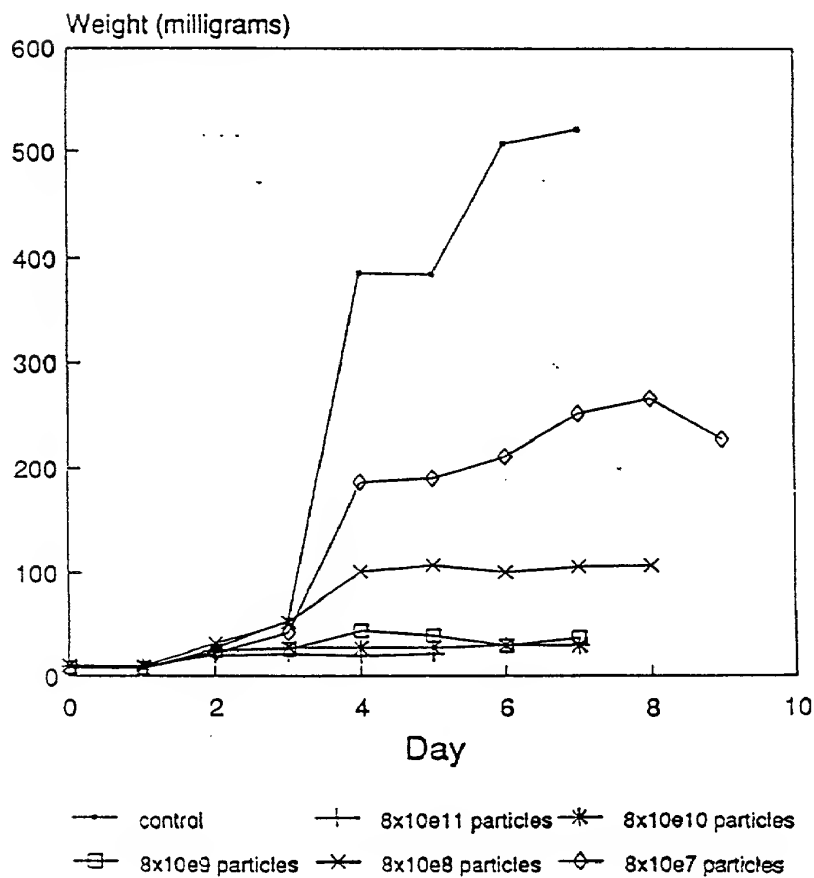
2170	2190	2210
TCCATCATCAAGTCCGTGGCGAGACTGCCGTGGCGGCTCAGTCCGGCCTCGCGAAG		
-----+	-----+	-----+
S I I K S V G E T A V G A A Q S G L A K		
2230	2250	2270
CTACCCGGACTGCTAATGAGTGTAACCAAGGAAGATTGCCGCGGTGTCCGCGCGCCGA		
-----+	-----+	-----+
L P G L L M S V P G K I A A R V R A R R		
2290	2310	2330
GCGCGCCGCGCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAA		
-----+	-----+	-----+
A R R R A A R A N *		
2350	2370	2390
AACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCGTCGTTAC		
-----+	-----+	-----+
2410	2430	2450
ACGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAGACGTAGTAGCTC		
-----+	-----+	-----+
2470		
TGCGTCCCTCGGGATACCA		
-----+		

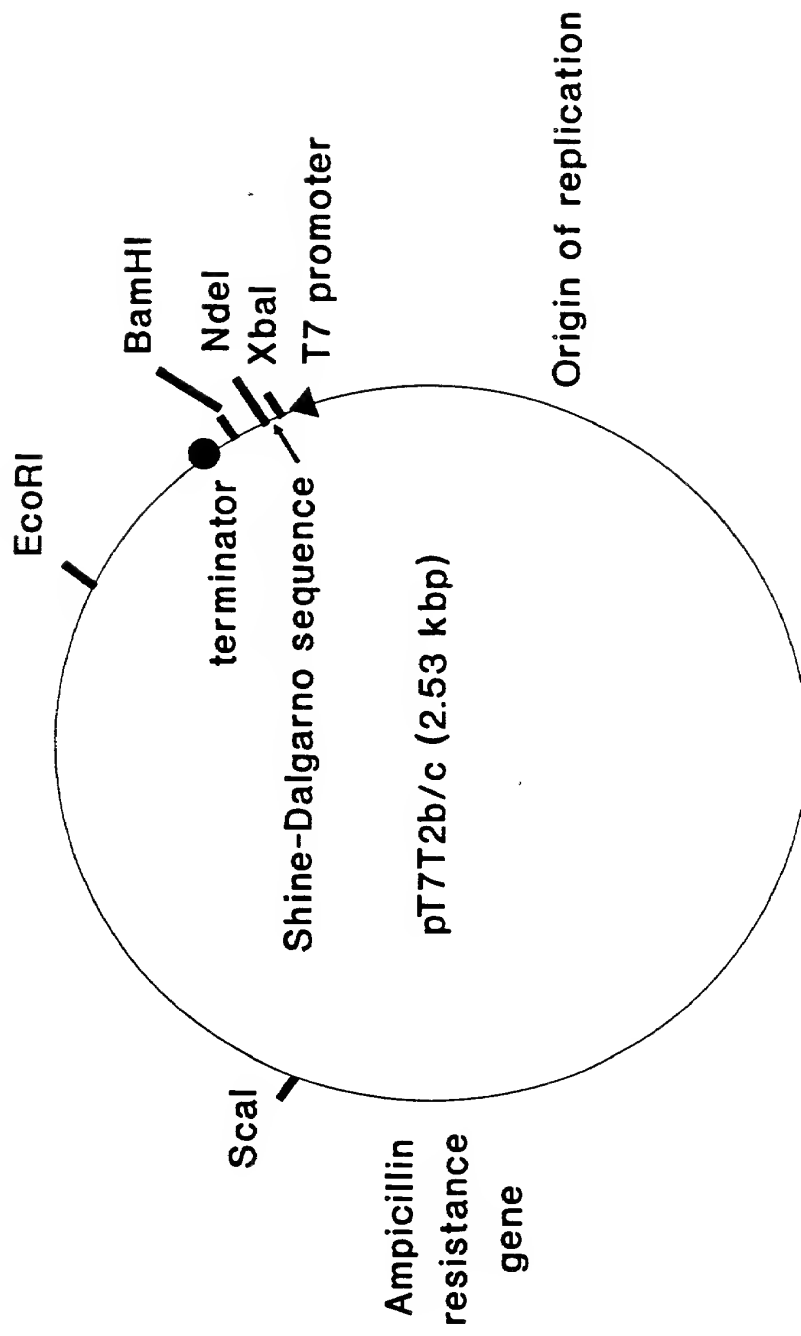
Fig. 3b (cont'd)

FIG. 4



B Weight gain of infected larvae





Proteins encoded by the HaSV genome

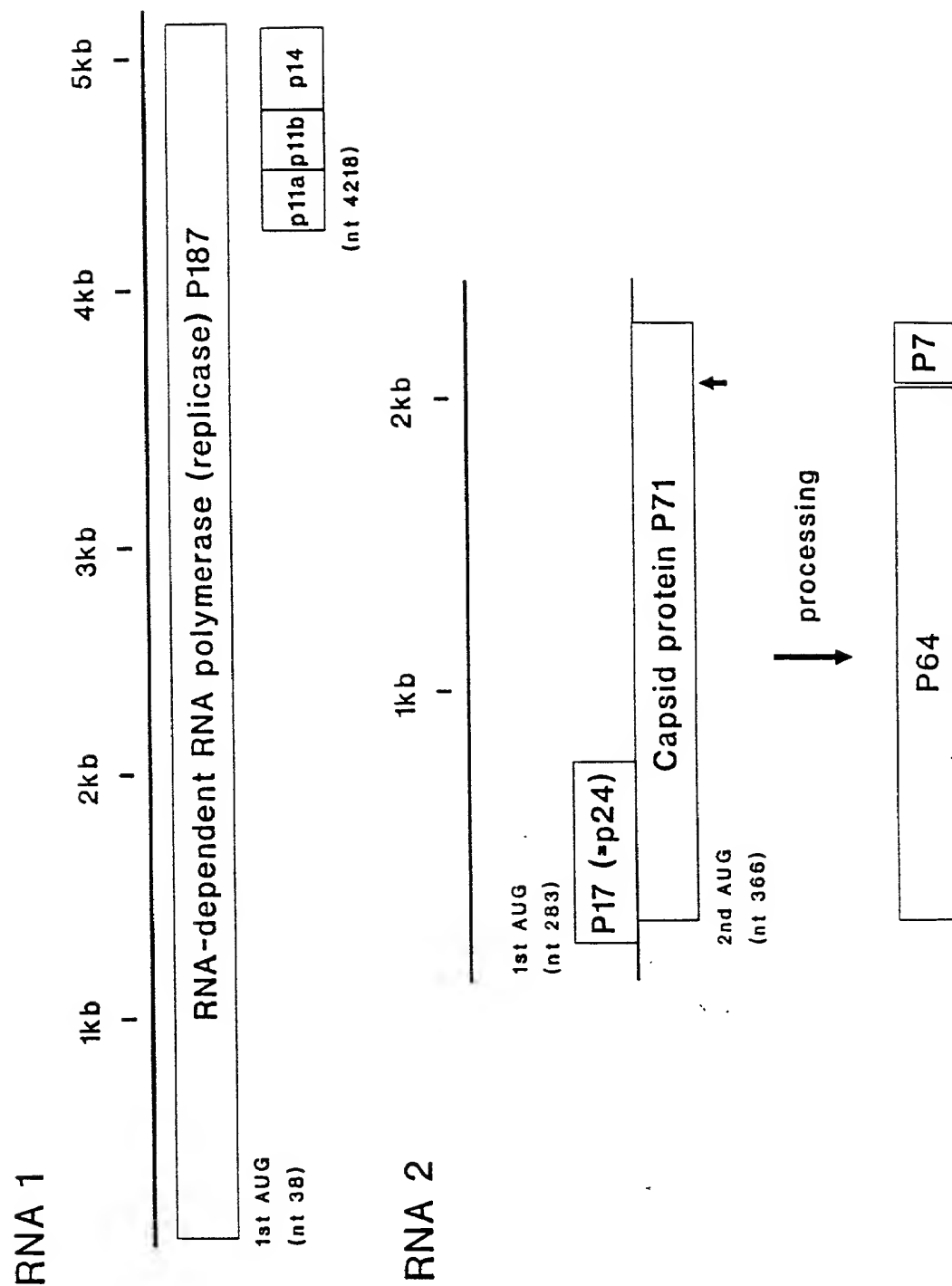


FIG. 6

PROTEINS EXPRESSED FROM HaSV RNA 2

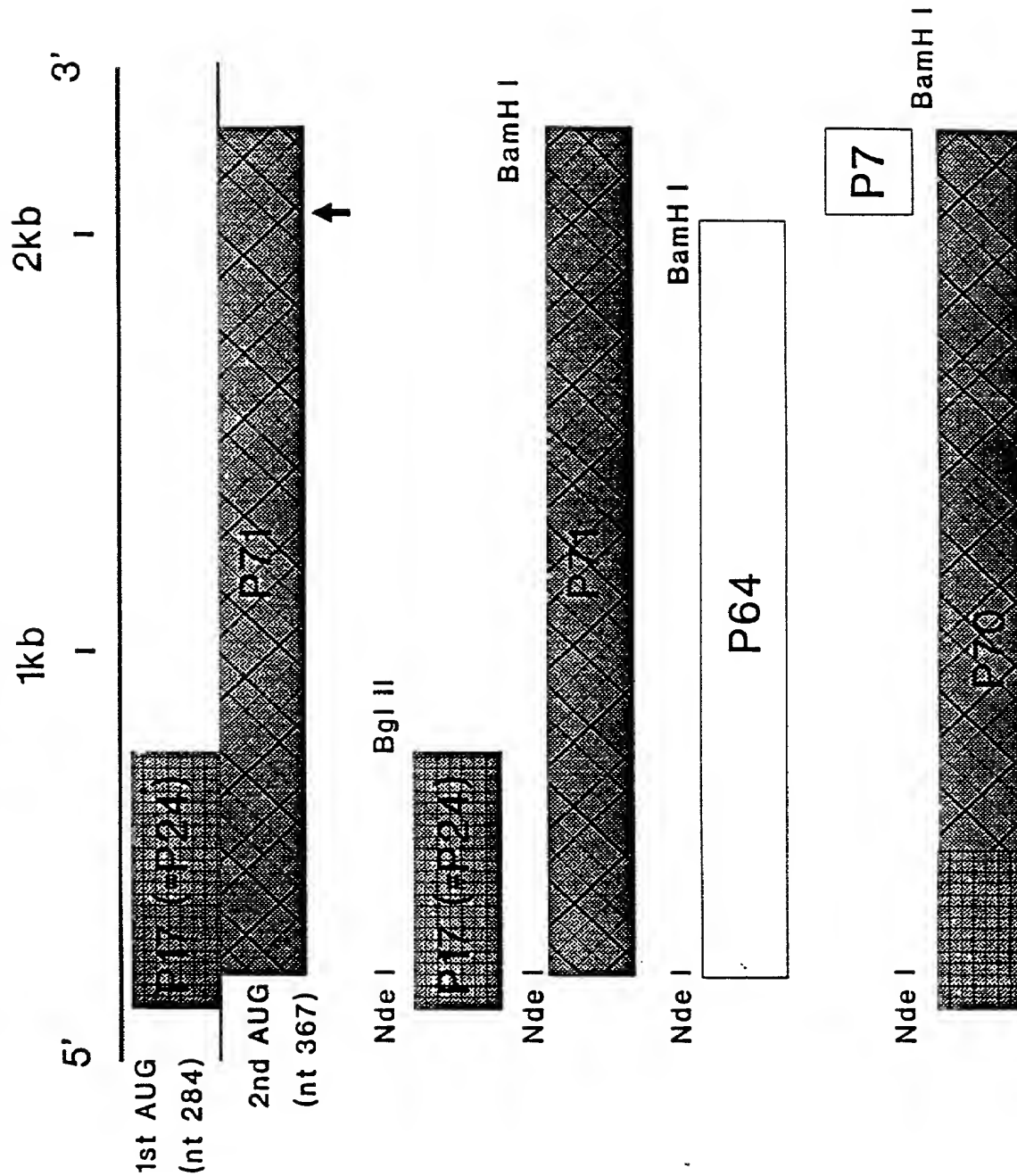
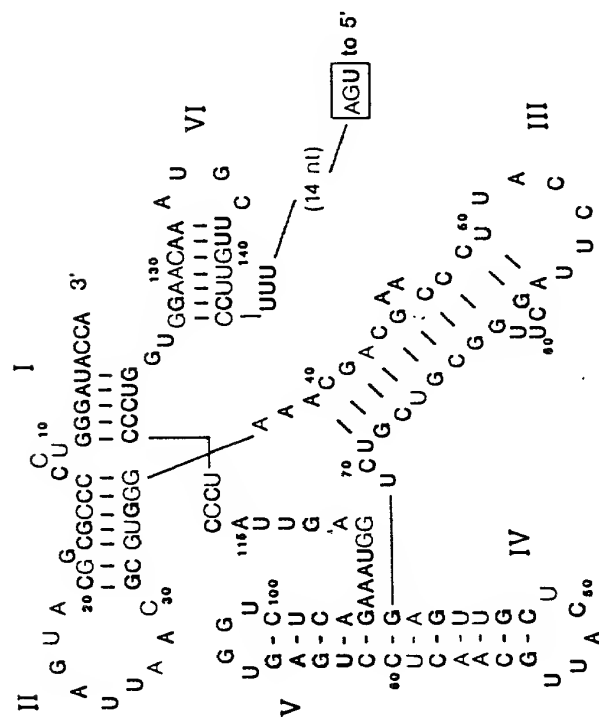


FIG. 7

HaSV RNA 3' - terminal tRNA-like structures

RNA 1



RNA 2

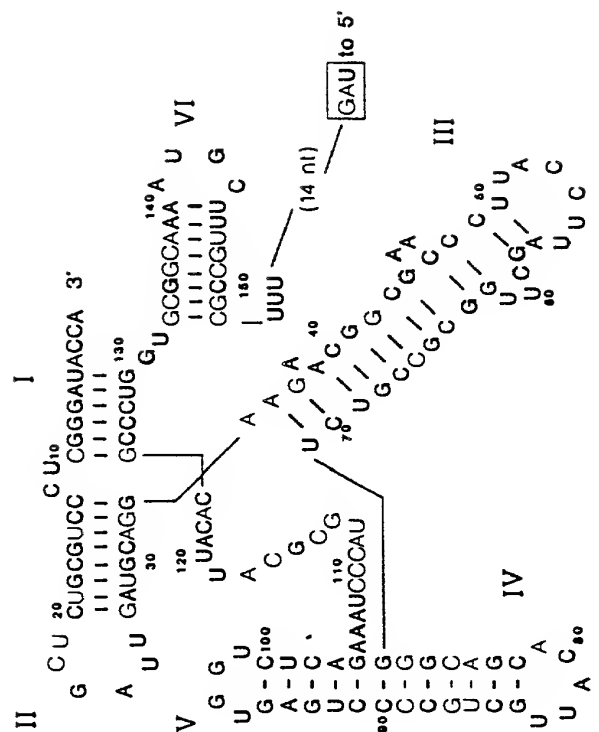
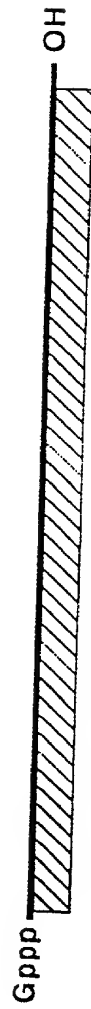
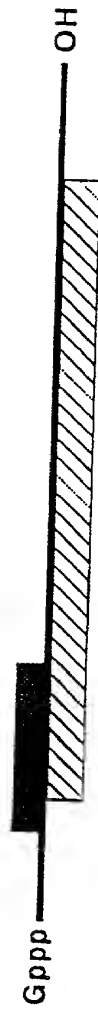


FIG. 8

HaSV RNA1



HaSV RNA2



Insect cell expression constructs

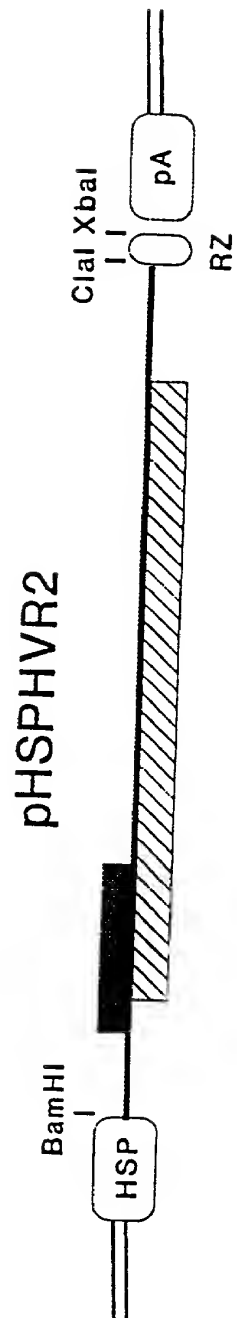
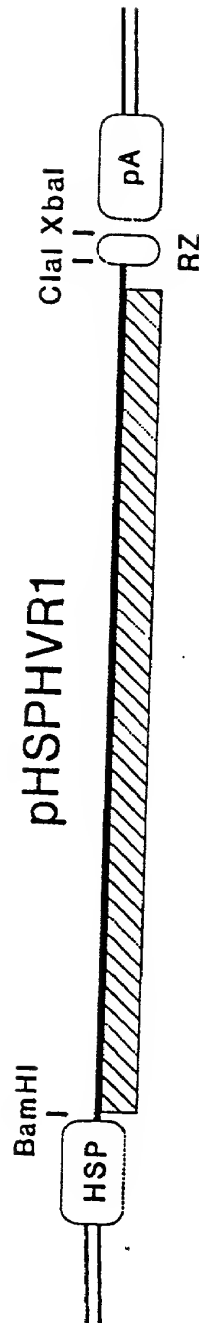
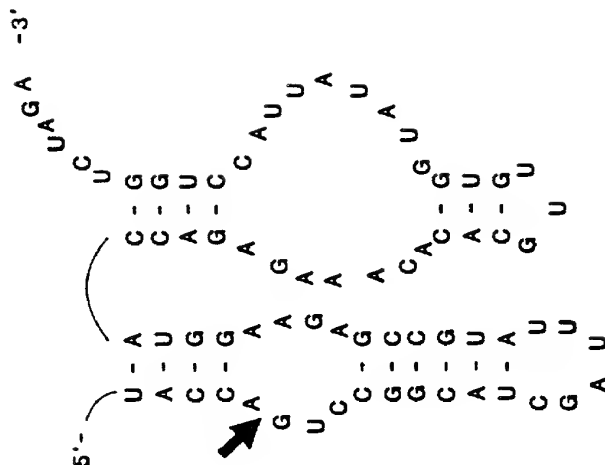


Fig. 9

CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

HAIRPIN



HEPATITIS DELTA VIRUS

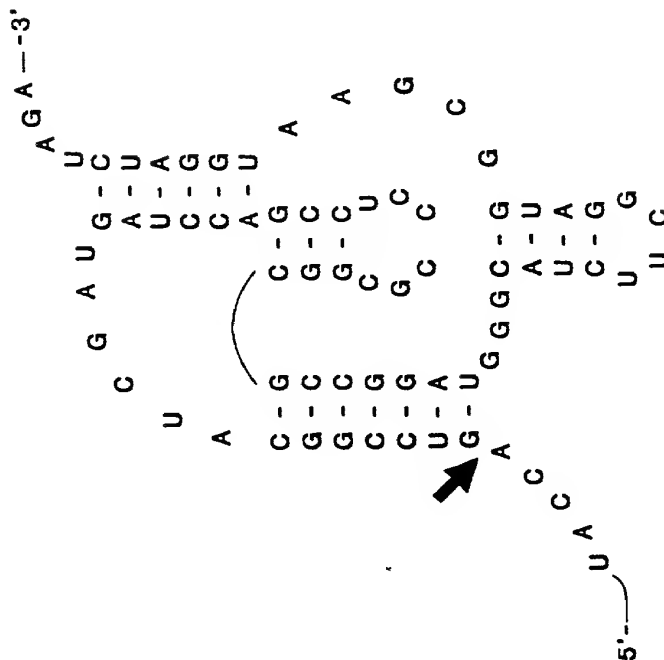
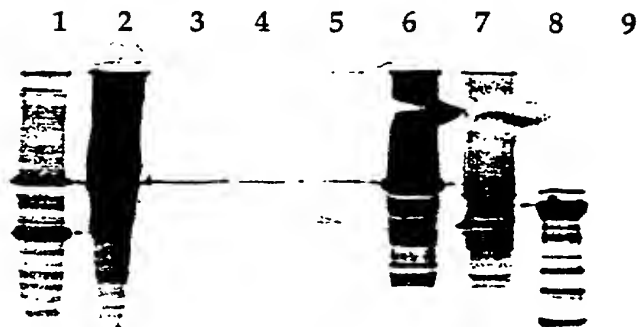


FIG. 10

FIG. 11

WESTERN BLOTS OF HaSV CAPSID PROTEIN

A. HaSV ANTISERUM



B. HaSV ANTISERUM



C. Bt ANTISERUM



Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.4	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.6	0.5	0	1
Depression score	0.4	0.5	0	1
Life satisfaction	0.7	0.5	0	1
Quality of life	0.8	0.4	0	1
Healthcare utilization	0.6	0.5	0	1
Health insurance status	0.9	0.3	0	1
Healthcare access	0.7	0.5	0	1
Healthcare cost	1000	300	500	2000
Healthcare quality	0.8	0.4	0	1
Healthcare satisfaction	0.7	0.5	0	1
Healthcare utilization frequency	0.5	0.5	0	1
Healthcare utilization cost	500	200	250	1000
Healthcare utilization quality	0.8	0.4	0	1
Healthcare utilization satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost	250	100	125	500
Healthcare utilization frequency quality	0.8	0.4	0	1
Healthcare utilization frequency satisfaction	0.7	0.5	0	1
Healthcare utilization cost quality	0.8	0.4	0	1
Healthcare utilization cost satisfaction	0.7	0.5	0	1
Healthcare utilization quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality	0.8	0.4	0	1
Healthcare utilization frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency quality satisfaction	0.8	0.4	0	1
Healthcare utilization cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization cost frequency satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization frequency quality cost satisfaction	0.8	0.4	0	1
Healthcare utilization frequency quality cost satisfaction	0.7	0.5	0	1
Healthcare utilization cost frequency quality satisfaction	0.8	0.4	0	1
Healthcare utilization cost frequency quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
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Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
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Healthcare utilization frequency cost quality satisfaction	0.8	0.4	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.5	0	1
Healthcare utilization quality frequency cost satisfaction	0.8	0.4	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.5	0	1
Healthcare utilization frequency cost quality satisfaction	0.			

CONT

1 2 3 4 5 6 7 8 9 10

A B C D E F G H

70

100

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.4	0	1
Exercise frequency	0.3	0.5	0	1
Stress level	0.6	0.5	0	1
Sleep quality	0.7	0.4	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.6	0.5	0	1
Depression score	0.4	0.5	0	1
Anxiety score	0.3	0.5	0	1
Resilience score	0.7	0.4	0	1
Self-efficacy score	0.6	0.5	0	1
Optimism score	0.5	0.5	0	1
Gratitude score	0.6	0.4	0	1
Forgiveness score	0.5	0.5	0	1
Empathy score	0.6	0.4	0	1
Compassion score	0.5	0.5	0	1
Kindness score	0.6	0.4	0	1
Generosity score	0.5	0.5	0	1
Patience score	0.6	0.4	0	1
Humility score	0.5	0.5	0	1
Modesty score	0.6	0.4	0	1
Shame score	0.5	0.5	0	1
Guilt score	0.4	0.5	0	1
Envy score	0.3	0.5	0	1
Jealousy score	0.2	0.5	0	1
Anger score	0.3	0.5	0	1
Dislike score	0.2	0.5	0	1
Disrespect score	0.1	0.5	0	1
Disapproval score	0.1	0.5	0	1
Discomfort score	0.1	0.5	0	1
Displeasure score	0.1	0.5	0	1
Disappointment score	0.1	0.5	0	1
Disillusion score	0.1	0.5	0	1
Disregard score	0.1	0.5	0	1
Disinterest score	0.1	0.5	0	1
Dislike score	0.1	0.5	0	1
Disrespect score	0.1	0.5	0	1
Disapproval score	0.1	0.5	0	1
Discomfort score	0.1	0.5	0	1
Displeasure score	0.1	0.5	0	1
Disappointment score	0.1	0.5	0	1
Disillusion score	0.1	0.5	0	1
Disregard score	0.1	0.5	0	1
Disinterest score	0.1	0.5	0	1

Fig. 13

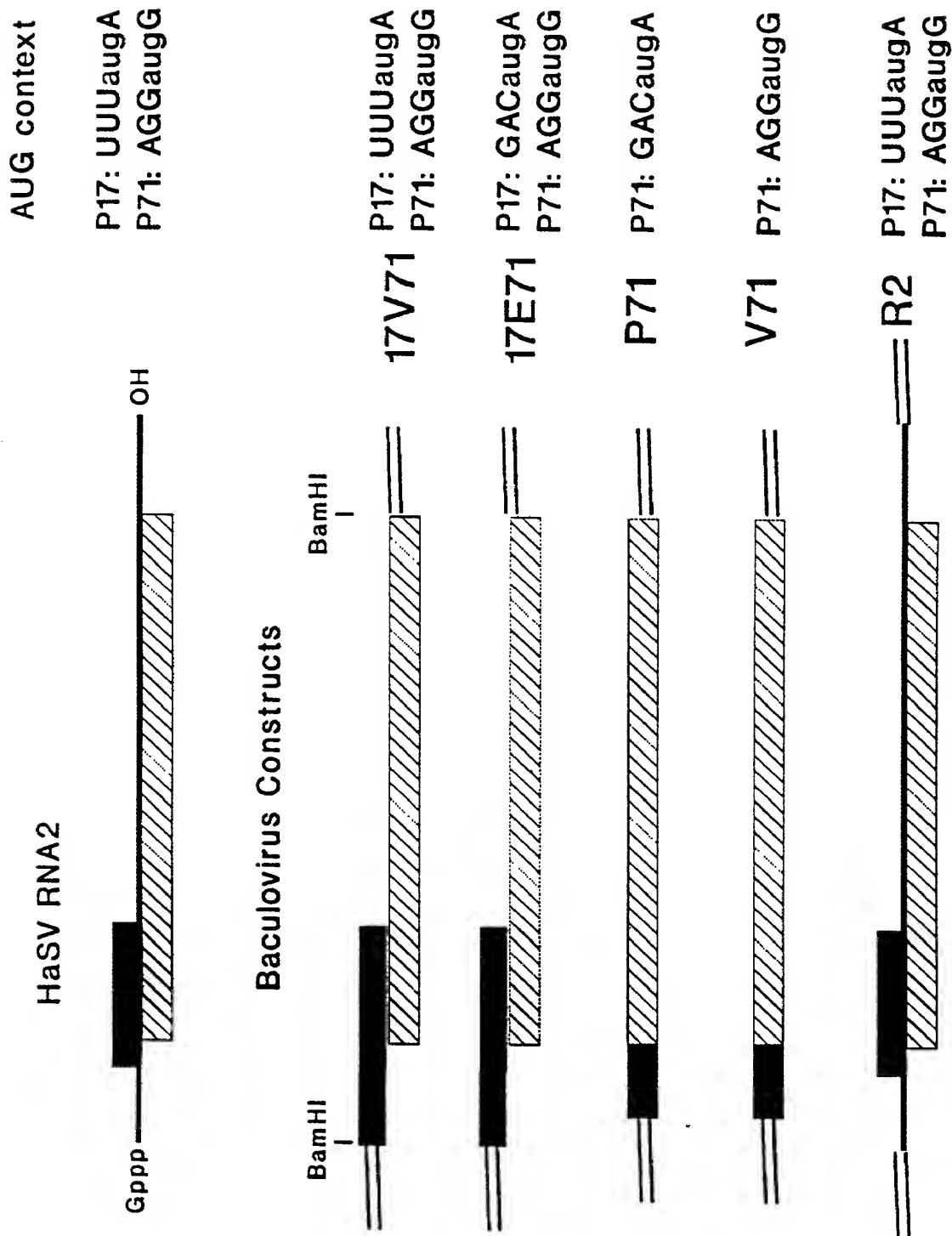


FIG. 14a

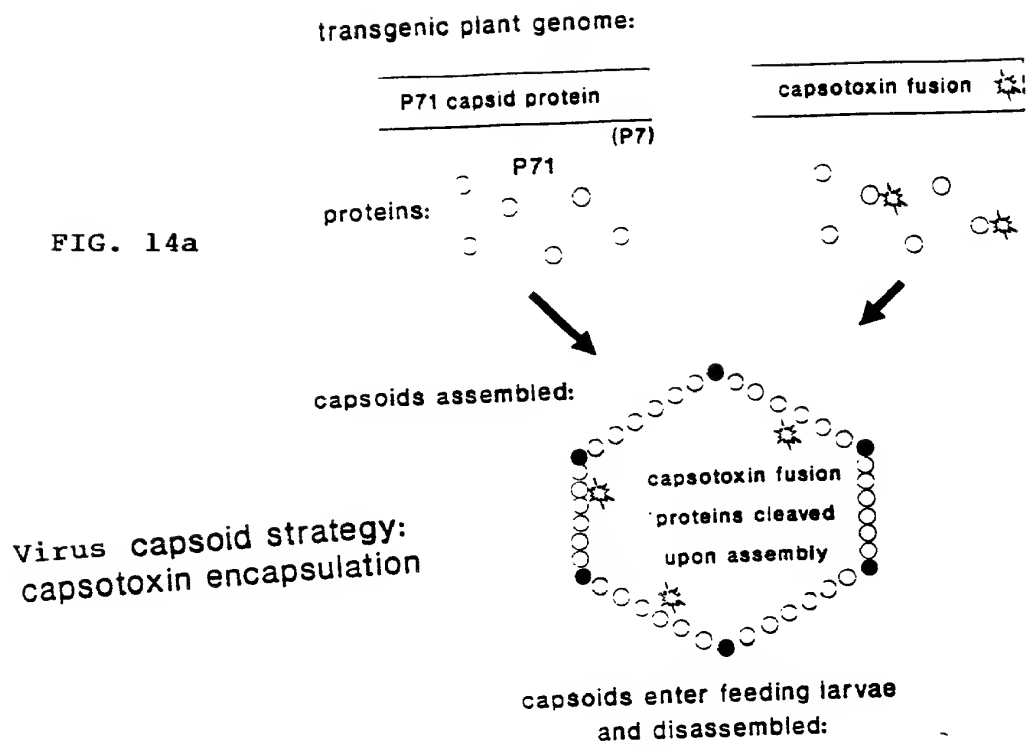
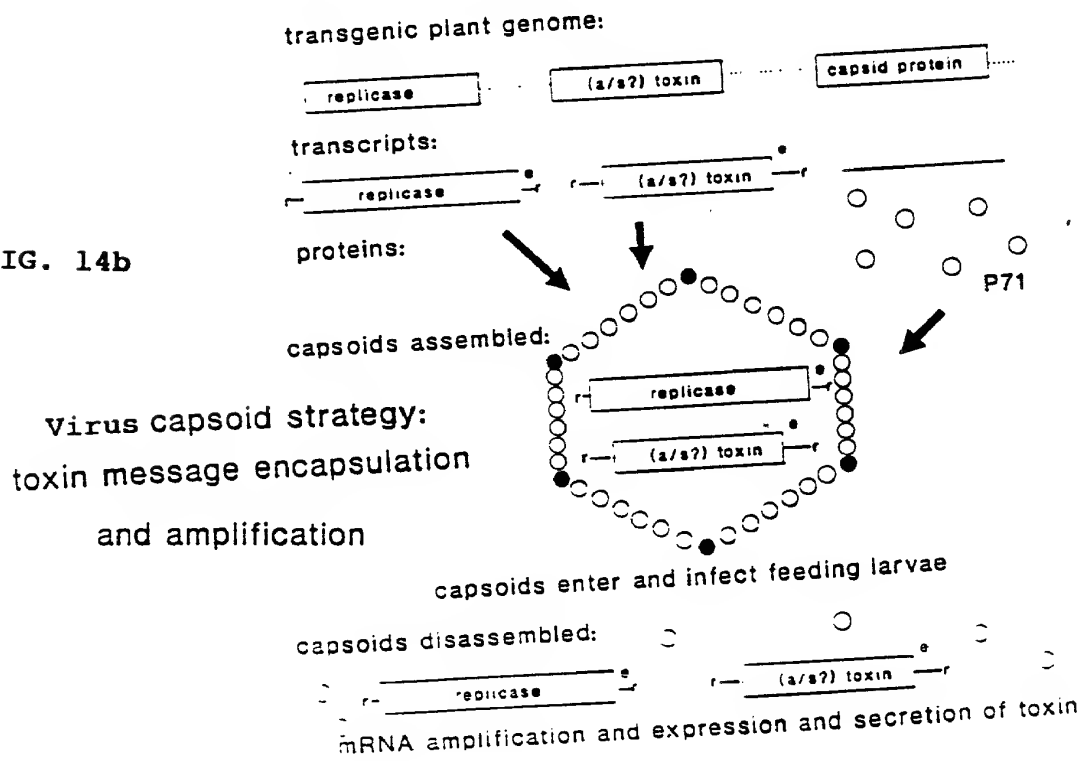


FIG. 14b



Virus expression in plants: the one-way vector

FIG. 14c

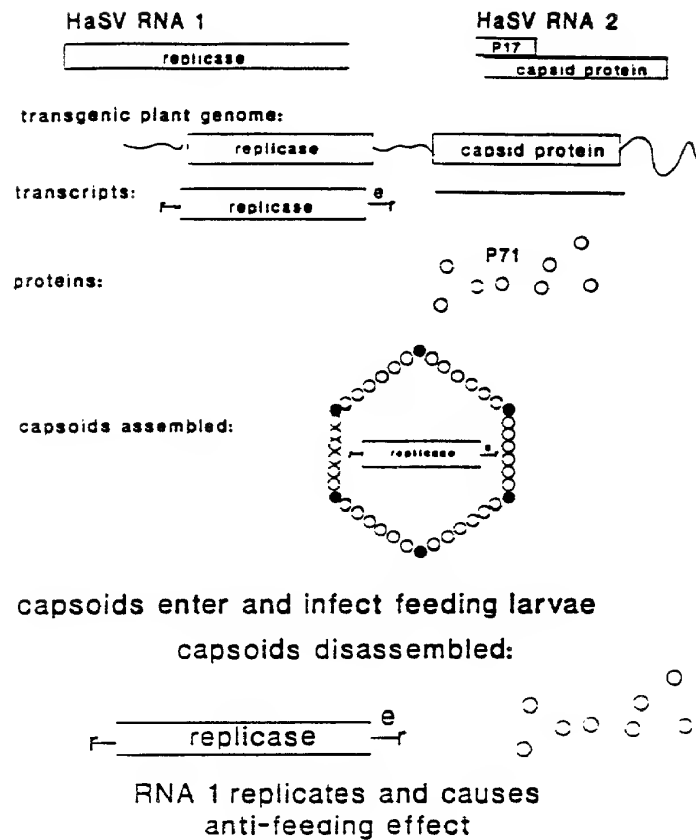
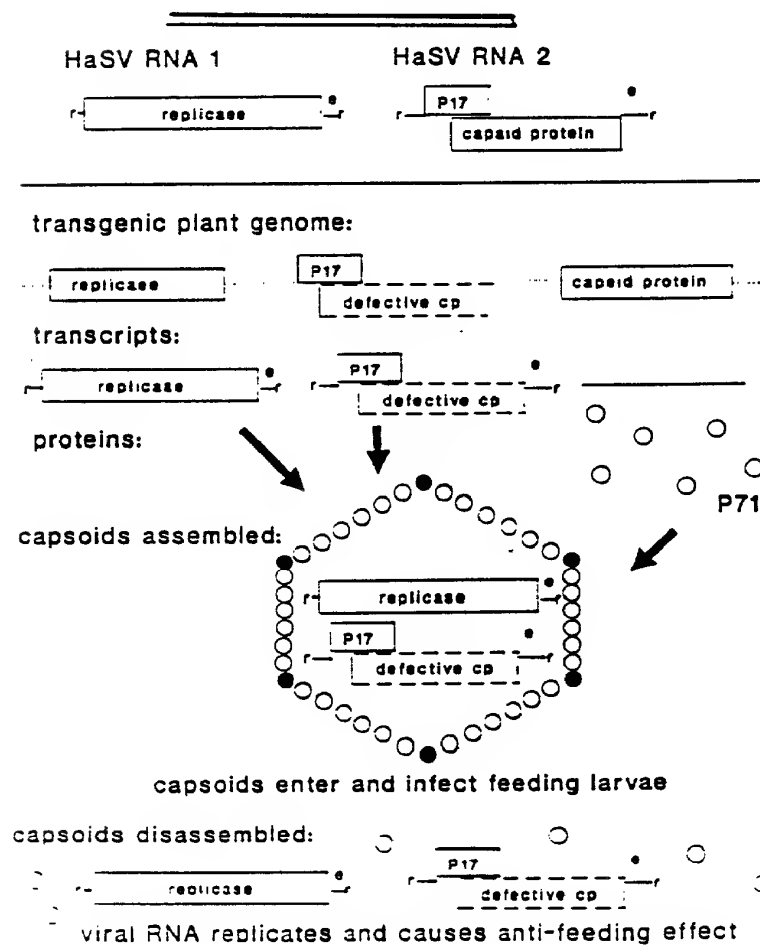
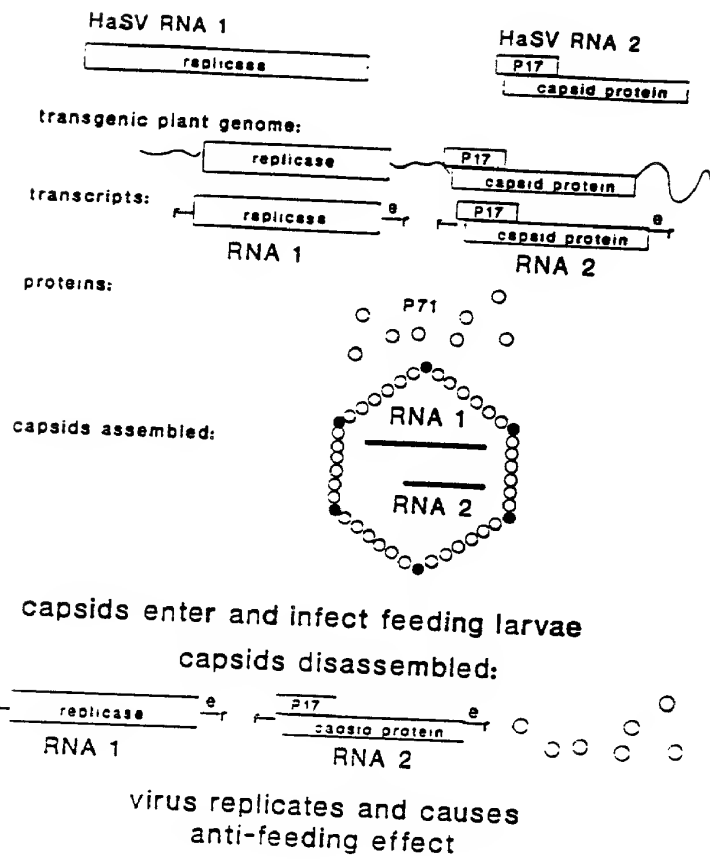


FIG. 14d



virus expression in plants:

FIG. 14e



virus expression in plants: the one-way vector for a toxin

FIG. 14f

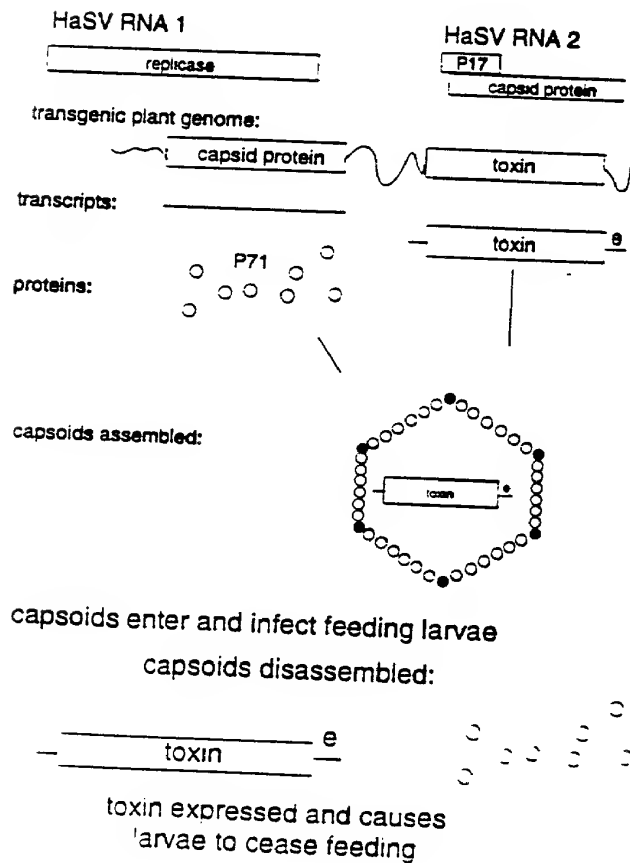


Fig. 15

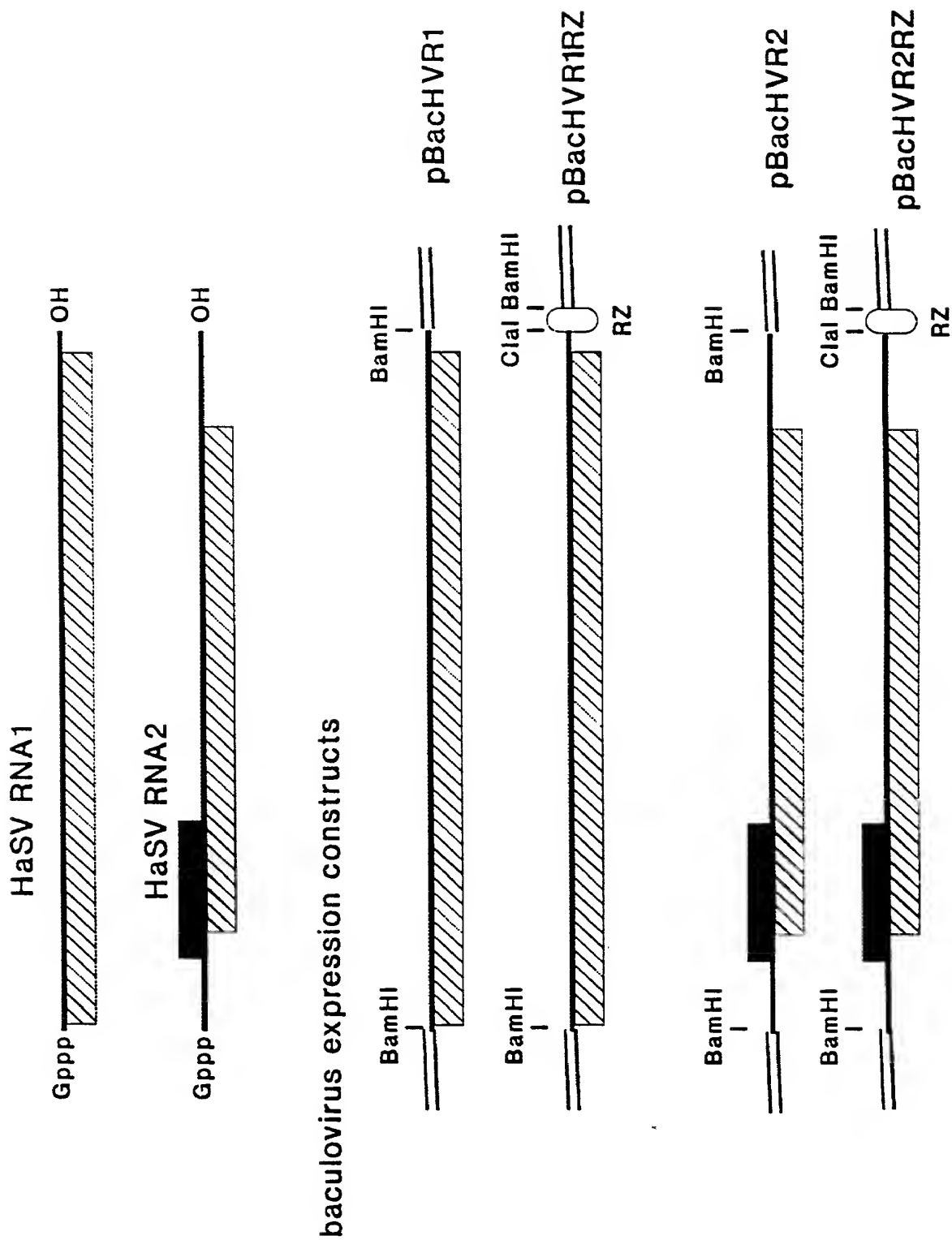
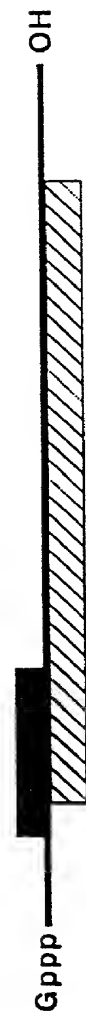


Fig. 16

HaSV RNA1



HaSV RNA2



Protoplast expression constructs

